



TRANSLATE of: raji9-1-1a.seq check: 6400 from: 88 to: 2575
generated symbols 1 to: 829.

Raji9-1-1A HBCK C nfirmmed Sequence
SR4364 Garka/Milne
file:[Bertlesj.Garka]Raji9-1-1A.seq

Raji9-1-1a.Pep Length: 825 [REDACTED] 10:07 Type: P Check: 1271

1 MSAPSEEEY ARLVMEAQPE WLRAEVKRLS HELAETTREK IQAAEYGLAV
51 LEEKHQLKLQ FEELEVDEYA IRSEMEQLKE AFGQAHTNHK KVAADGESRE
101 ESLIQESASK EQYYVRKYLE LQTELKQLRN VLTNTQSENE RLASVAQELK
151 EINQNVEIQR GRLRDDIKEY KFREARLLQD YSELEENIS LQKQVSVLRQ
201 NQVEFEGLKH EIKRLEEETE YLNSQLEDAI RLKEISERQL EEALETLKTE
251 REQNSLRKE LSHYMSINDS FYTSHLHVSL DGLKFSDDAE EPNNDAEALV
301 NGFEHGLAK LPLDNKTSTP KKEGLAPPSP SLVSDLLSEL NISEIQKLKQ
351 QLMQMERKA GLLATLQDTQ KQLEHTRGSL SEQQEKVTRL TENLSALRRL
401 QASKERQTAL DNEKDRDSHE DGDYVEVDIN GPEILACKYH VAVAEAGELR
451 EQLKALRSTH EAREAQAEE KGRYEAEGQA LTKVSLLEK ASRQDRELLA
501 RLEKELKKVS DVAGETQGSL SVAQDELVTF SEELANLYHH VCMCNNETPN
551 RVMLDYYREG QGGAGRTSPG GRTSPEARGR RSPILLPKGL LAPEAGRADG
601 GTGDSSPSPG SSLPSPLSDP RREPMNIYNL IAIIRDQIKH LQAAVDRTTE
651 LSRQRIASQE LGPAVDKDKE ALMEEILKLK SLLSTKREI TTLRTVLKAN
701 KQTAEVALAN LKSKYENKA MYTETMMKLK NELKALKEDA ATFSSLRAMF
751 ATRCDEYITQ LDEMQRQLAA AEDEKKTLS LLRMAIQKL ALTQRLELLE
801 LDHEQTRRGR AKAAPKTKPA TPSL*

Raji9-1-1A HBCK Confirmed Sequence
SR4364 Garka/Milne
file:[Bertlesj.Garka]Raji9-1-1A.seq

Raji9-1-1a.Seq Length: 3345 15:04 Type: N Check:
6400 ..

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1  aaaaagcaaa agaattcgcg gccgcGCGGC TGAGGAGGGC CCGGCCTGCG
51  AGAGCCTCAG TGGGAGCCGG CTCAGCCCTC GGCCACCATG TCGGCGCCGT
101 CGGAGGAGGA GGAGTACGCG CGGCTGGTGA TGGAGGCGCA GCCGGAGTGG
151 CTGCGCGCCG AGGTGAAGCG GCTGTCCAC GAGCTGGCCG AGACCACGCG
201 TGAGAAGATC CAGGCGGCCG AGTACGGGCT GGCGGTGCTC GAGGAGAAGC
251 ACCAGCTCAA GCTGCAGTTC GAGGAGCTCG AGGTGGACTA TGAGGCTATC
301 CGCAGCGAGA TGGAGCAGCT CAAGGAGGCC TTTGGACAAG CACACACAAA
351 CCACAAGAAG GTGGCTGCTG ACGGAGAGAG CCGGGAGGAG AGCCTGATCC
401 AGGAGTCGGC CTCCAAGGAG CAGTACTACG TCGGGAAGGT GCTAGAGCTG
451 CAGACGGAGC TGAAGCAGTT GCGCAATGTC CTCACCAACA CGCAGTCGGA
501 GAATGAGCGC CTGGCCTCTG TGGCCCAGGA GCTGAAGGAG ATCAACCAGA
551 ATGTGGAGAT CCAGCGTGGC CGCCTGCGGG ATGACATCAA GGAGTACAAA
601 TTCCGGGAAG CTCGTCTGCT GCAGGACTAC TCGGAACTGG AGGAGGAGAA
651 CATCAGCCTG CAGAAGCAAG TGTCTGTGCT CAGACAGAAC CAGGTGGAGT
701 TTGAGGGCCT CAAGCATGAG ATCAAGCGTC TGGAGGAGGA GACCGAGTAC
751 CTCAACAGCC AGCTGGAGGA TGCCATCCGC CTCAAGGAGA TCTCAGAGCG
801 GCAGCTGGAG GAGGCGCTGG AGACCCTGAA GACGGAGCGC GAACAGAAGA
851 ACAGCCTGCG CAAGGAGCTG TCACACTACA TGAGCATCAA TGA CTCCTTC
901 TACACCAGCC ACCTGCATGT CTCGCTGGAT GGCCTCAAGT TCAGTGACGA
951 TGCTGCCGAG CCCAACAACG ATGCCGAGGC CCTGGTCAAT GGCTTTGAGC
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1001 ACGGCGGCCT GGCCAAGCTG CCACTGGACA ACAAGACCTC CACGCCCCAAG
1051 AAGGAGGGCC TCGCACCGCC CTCCTCCAGC CTCGTCTCCG ACCTACTCAG
1101 TGAGCTCAAC ATCTCTGAGA TCCAGAAGCT GAAGCAGCAG CTGATGCAGA
1151 TGGAGCGGGA AAAGGCGGGC CTGCTGGCAA CGCTGCAGGA CACACAGAAG
1201 CAGCTGGAGC ACACGCGGGG CTCCTGTCA GAACAGCAGG AGAAGGTGAC
1251 CCGCCTCACA GAGAATCTGA GTGCCCTGCG GCGCCTGCAG GCCAGCAAGG
1301 AGCGGCAGAC AGCCCTGGAC AACGAGAAGG ACCGTGACAG CCATGAGGAT
1351 GGGGACTACT ACGAGGTGGA CATCAACGGG CCTGAGATCT TGGCCTGCAA
1401 GTACCATGTG GCTGTGGCTG AGGCTGGCGA GCTCCGCGAG CAGCTCAAGG
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1751 ACTACTACCG CGAGGGCCAG GCGGGGGCCG GCCGCACCAG TCCCGGGGGC
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1851 GGGGCTGCTG GCTCCTGAGG CGGGCCGAGC AGATGGTGGG ACGGGGGACA
1901 GCAGCCCCCTC GCCTGGCTCC TCACTGCCAT CACCCCTGAG TGACCCACGC
1951 CGGGAGCCCA TGAACATCTA CAACCTGATC GCTATCATCC GTGACCAGAT
2001 CAAGCACCTG CAGGCAGCCG TGGACCGCAC CACGGAGCTG TCACGCCAGC
2051 GCATTGCCTC TCAGGAGCTG GGCCCCGCGG TGGACAAGGA CAAGGAAGCG
2101 CTTATGGAGG AGATCCTCAA GCTGAAGTCG CTGCTCAGCA CCAAGCGGGA

2151 GCAGATCACC ACGCTGCGCA CTGTGCTCAA GGCCAACAAG CAGACGGCCG
2201 AGGTGGCCCT TGCCAACCTG AAGAGCAAGT ATGAGAATGA GAAGGCCATG
2251 GTTACCGAGA CCATGATGAA GCTGCGCAAT GAGCTCAAGG CCCTCAAGGA
2301 GGACGCAGCC ACCTTCTCCT CGCTGCGTGC TATGTTTGCC ACCAGGTGTG
2351 ACGAGTACAT TACACAGCTG GATGAGATGC AGCGGCAGCT GCGCGCTGCT
2401 GAGGACGAGA AGAAGACGCT GAACTCGCTG CTGCGCATGG CCATCCAGCA
2451 GAAGCTGGCG CTGACCCAGC GGCTGGAGCT GCTCGAGCTG GACCATGAGC
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2551 CCGAGCCTGT AGAGTAGCTG CCAGGAGGAC TTGGCCACCC GGCCCTGTCA
2601 CACTGCAGCC CTTTCCCCTT CCCTCTCGTG GCCCACAAGG AGGAAGGAAG
2651 GGCAACCTAA AAGCCCACTT AGAAACTTTT TGGATATGCC ACTGCAATTC
2701 TTTTCAAAT AGCATTCCCC AGGTTTTTAA TGGGAGGAAA AAAAGCTTTA
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2951 CGTAGAGACG GTCTCAGGTG CCGTGGTCTA TGCTCGTGGT CCTGTAGCTG
3001 TCCGCCTCAG CTCCCACCGT GTTTGTCTGG TGTCAGCACG AGGCAGAGCT
3051 GTGTGCTCCA TAGCGTGTAG CTTTAGACTC GGAGATGAGT GCTTTGACCC
3101 AGCGAGGAGC TCAGCTAAGT GTATCCACGC TGTGGTTCAG CAGCCTTAG
3151 ATCATACGGC ATTGTGGTTC ATGTTTGAAA TTACAGATTT TAAATGCCAT
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3251 TTATTATTAT TCTTAGGAAT AGTTCAATGT AACAAGAAGA AAACCTTGACC

3301 TTTGCTCTGG TAAAAACAGT AATAgcggcc gcgaattcag cttgg